The effect of L. acidophilus NCFM intake on insulin sensitivity and gut microbiota

a randomized placebo-controlled trial

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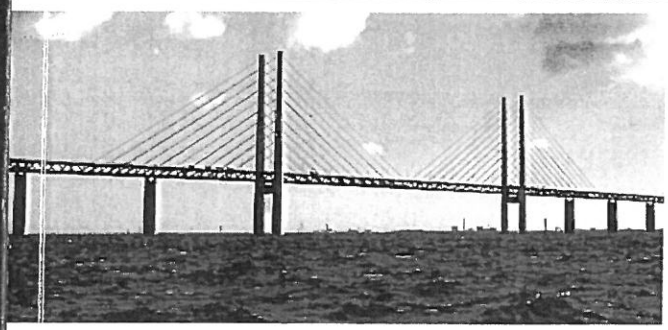
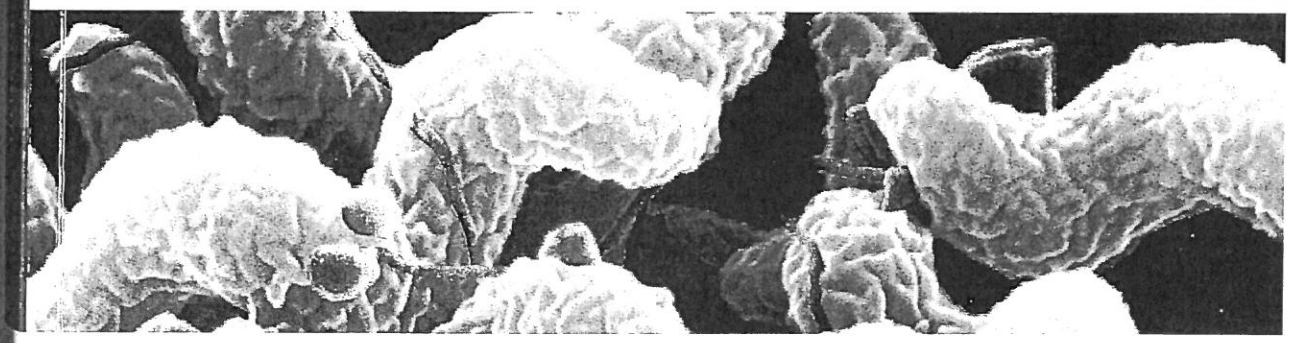


Copenhagen 30th August - 3rd September



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PSE1.03 The effect of *L. acidophilus* NCFM intake on insulin sensitivity and gut microbiota: a randomized placebo-controlled trial

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Recent studies indicate that there is a link between gut microbial composition and metabolic diseases such as obesity and diabetes type 2. Furthermore, according to animal studies, intake of probiotic bacteria may improve glucose homeostasis. We hypothesised that (i) the gut microbiota (GM) contributes to glucose tolerance and insulin resistance and (ii) the intake of probiotic bacteria affects the GM composition and improve insulin sensitivity by attenuating systemic inflammation. The effect of oral supplementation with the probiotic bacterium *L. acidophilus* NCFM on the insulin sensitivity, inflammatory response and GM composition was investigated in a double-blinded randomised human trial. The trial included 45 males with type 2 diabetes, impaired or normal glucose tolerance allocated to a four-week treatment course with either NCFM or placebo. Insulin sensitivity, estimated by the hyperinsulinaemic euglycaemic clamp, was preserved among the individuals in the NCFM group, whereas it decreased in the placebo group. Both baseline inflammatory markers (C-reactive protein, TNF, IL-6 and IL-1) and the systemic inflammatory response, induced by injection of *E. coli* lipopolysaccharides, were unaffected by the intervention. The GM composition was examined by denaturating gradient gel electrophoresis (DGGE), real-time PCR and in a subgroup of subjects by 454 FLX pyrosequencing of the V4 region of 16S rRNA gene. The proportions of phylum *Firmicutes* and class *Clostridia* were significantly reduced in the diabetic group compared to the control group. Furthermore, the ratios of *Bacteroidetes* to *Firmicutes* as well as the ratios of *Bacteroides-Prevotella* group to *C. coccoides-E. rectale* group correlated positively and significantly with plasma glucose concentration. Similarly, class *Betaproteobacteria* was highly enriched in the diabetic persons and positively correlated with plasma glucose. Intake of *L. acidophilus* NCFM did not affect the DGGE profiles and the proportions of the main bacterial populations (*Bacteroides, C.leptum, C.coccoides- E. rectale, Prevotella, Roseburia*) in the GM. In conclusion, the results of this study indicate that type 2 diabetes in humans is associated with compositional changes in the intestinal microbiota. Furthermore, compared to placebo, four weeks intake of *L. acidophilus* NCFM preserves insulin sensitivity, but does not affect the systemic inflammatory response.

PSE1.04 Probiotics and prebiotics in poultry feeding: a strategy to reduce the transmission of C. *jejuni* along the food chain

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With the ban of dietary antimicrobial agents, the use of probiotics (PRO) and prebiotics (PRE) has attracted a great deal of attention in order to improve intestinal health and control food-borne pathogens, which is an important concern for the production of safe meat and meat products. *Campylobacter jejuni* has now emerged as a leading bacterial cause of food-borne gastroenteritis in humans around the world, and epidemiological evidence indicates poultry and poultry products as a significant source of human infection.
In this work we evaluated the capability of probiotics and prebiotics to modulate the gut microbiota of broiler chickens to obtain a competitive reduction of *C. jejuni* colonization. PRO treatment: 2 probiotic strains (*B. longum* PCB133 and *L. plantarum* PCS20) were separately administered to 16 broiler chickens by oral gavage (~ 10^8 cfu/day) for 15 days. PRE treatment: 2 prebiotic compounds (FOS and GOS) were separately administered to 14 broilers mixed with normal feed at a concentration respectively of 0.5% and 3%. The faecal samples were collected from 10 broilers in each group. Detection and quantification of the targeted bacterial groups (*Bifidobacterium* spp., *Lactobacillus* spp., *Campylobacter* spp., *B. longum*, *L. plantarum* and *C. jejuni*) were performed by Real-Time PCR using SybrGreen chemistry. In PRO treatment *B. longum* was recovered in the faeces of all animals (~ 4 $\log_{10}$ cfu/g of faeces) while *L. plantarum* was not present at detectable concentration after 15 days of supplementation. *C. jejuni* concentration in poultry faeces was significantly ($p<0.05$) reduced in chickens administered with *B. longum* PCB133. In PRE treatment a significant ($p<0.05$) increase in *Bifidobacterium* spp was observed in GOS group, as compared with FOS group, coupled with a decrease ($p<0.05$) of *Campylobacter* spp. *C. jejuni* was not present in broilers used for PRE treatment. There were no significant differences regarding animal weight and feed intake between groups. The results obtained in this study indicate that suitable probiotic and prebiotic supplements can be selected and used to develop an effective synbiotic formula for poultry feed.

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PSE1.05 Effects of whey

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interesting, as they play a role i
tive evaluation of the changes
functional food intake may aid
management of CMP allergy.

PSE1.06 Gut microbiota a

Andrea Gianotti (1
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(1) Alma Mater Stu
(2) Alma Mater Stu

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